

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

10/577,679
JFWO
05/11/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/577, 679

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."~~
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,679

TIME: 10:58:07

Input Set : A:\31831 Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577679.raw

3 <110> APPLICANT: Hardy, Britta
 4 Battler, Alexander
 5 Raiter, Annat
 6 Kornowski, Ran
 7 Weiss, Chana
 9 <120> TITLE OF INVENTION: ANGIOGENIC PEPTIDES AND USES THEREOF
 11 <130> FILE REFERENCE: 31831
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/577,679
 C--> 13 <141> CURRENT FILING DATE: 2006-04-28
 13 <160> NUMBER OF SEQ ID NOS: 32
 15 <170> SOFTWARE: PatentIn version 3.2

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

499 <210> SEQ ID NO: 32
 500 <211> LENGTH: 7
 501 <212> TYPE: PRT
 502 <213> ORGANISM: Artificial sequence
 504 <220> FEATURE:
 505 <223> OTHER INFORMATION: A conserved sequence motif
 508 <220> FEATURE:
 509 <221> NAME/KEY: misc_feature
 510 <222> LOCATION: (3)..(6)
 511 <223> OTHER INFORMATION: Any amino acid
 513 <400> SEQUENCE: 32
 W--> 515 Pro Trp Xaa Xaa Xaa Xaa Tyr
 516 1 5
 E--> 522 7

What is the
 Source of genetic
 Material. Pls
 See Stern # 11
 on Error Summary
 Sheet.

pls delete

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/577,679

DATE: 05/11/2006

TIME: 10:58:08

Input Set : A:\31831 Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577679.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:522 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32

STATISTICS SUMMARY

PATENT APPLICATION: US/10/577,679

DATE: 05/11/2006

TIME: 10:58:08

Input Set : A:\31831 Sequence Listing.txt

Output Set: N:\CRF4\05112006\J577679.raw

Application Serial Number: US/10/577,679

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 04-28-2006

Art Unit: IFWP

Software Application: PatentIN3.2

Total Number of Sequences: 32

Total Nucleotides: 481

Total Amino Acids: 380

Number of Errors: 1

Number of Warnings: 3

Number of Corrections: 2

MESSAGE SUMMARY

270 C: 1 (Current Application Number differs)

271 C: 1 (Current Filing Date differs)

332 E: 1 ((32) Invalid/Missing Amino Acid Numbering)

341 W: 3 ((46) "n" or "Xaa" used)